



September 19, 2002

## APPLICATION SERIAL NUMBER

**09902481**

**DOES NOT COMPLY WITH THE  
SEQUENCE RULES. See reasons below.**

**CRF, paper copy of sequence listing and  
statement that both are same missing.**

**The sequences disclosed on page 29, lines 1-7, of the specification need to be in CRF and paper copy of the sequence listing, but are missing.**

A handwritten signature in cursive script that appears to read "Kevin".



#14

## SEQUENCE LISTING

<110> Springer, Timothy  
Shimaoka, Motomu  
Shifman, Julia  
Mayo, Stephen

<120> NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY

<130> A-70586-1/RFT/RMS/RMK

<140> US 09/902,481  
<141> 2001-07-09

<150> US 60/216,600  
<151> 2000-07-07

<160> 13

<170> PatentIn version 3.1

<210> 1  
<211> 1153  
<212> PRT  
<213> Homo sapiens

<220>  
<221> mat\_peptide  
<222> (17)..()  
<223>

<400> 1

Met Ala Leu Arg Val Leu Leu Leu Thr Ala Leu Thr Leu Cys His Gly  
-15 -10 -5 -1

Phe Asn Leu Asp Thr Glu Asn Ala Met Thr Phe Gln Glu Asn Ala Arg  
1 5 10 15

Gly Phe Gly Gln Ser Val Val Gln Leu Gln Gly Ser Arg Val Val Val  
20 25 30

Gly Ala Pro Gln Glu Ile Val Ala Ala Asn Gln Arg Gly Ser Leu Tyr  
35 40 45

Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val  
50 55 60

Pro Val Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Thr  
65 70 75 80

Thr Ser Pro Pro Gln Leu Leu Ala Cys Gly Pro Thr Val His Gln Thr  
85 90 95

Cys Ser Glu Asn Thr Tyr Val Lys Gly Leu Cys Phe Leu Phe Gly Ser  
100 105 110

Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys  
115 120 125

Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser  
130 135 140

Ile Ile Pro His Asp Phe Arg Arg Met Lys Glu Phe Val Ser Thr Val  
145 150 155 160

Met Glu Gln Leu Lys Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr  
165 170 175

Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn  
180 185 190

Pro Asn Pro Arg Ser Leu Val Lys Pro Ile Thr Gln Leu Leu Gly Arg  
195 200 205

Thr His Thr Ala Thr Gly Ile Arg Lys Val Val Arg Glu Leu Phe Asn  
210 215 220

Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Val Val Ile  
225 230 235 240

Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile  
245 250 255

Pro Glu Ala Asp Arg Glu Gly Val Ile Arg Tyr Val Ile Gly Val Gly  
260 265 270

Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Ile Ala  
275 280 285

Ser Lys Pro Pro Arg Asp His Val Phe Gln Val Asn Asn Phe Glu Ala  
290 295 300

Leu Lys Thr Ile Gln Asn Gln Leu Arg Glu Lys Ile Phe Ala Ile Glu

305

310

315

320

Gly Thr Gln Thr Gly Ser Ser Ser Ser Phe Glu His Glu Met Ser Gln  
325 330 335

Glu Gly Phe Ser Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr  
340 345 350

Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys  
355 360 365

Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn  
370 375 380

Asp Ala Tyr Leu Gly Tyr Ala Ala Ala Ile Ile Leu Arg Asn Arg Val  
385 390 395 400

Gln Ser Leu Val Leu Gly Ala Pro Arg Tyr Gln His Ile Gly Leu Val  
405 410 415

Ala Met Phe Arg Gln Asn Thr Gly Met Trp Glu Ser Asn Ala Asn Val  
420 425 430

Lys Gly Thr Gln Ile Gly Ala Tyr Phe Gly Ala Ser Leu Cys Ser Val  
435 440 445

Asp Val Asp Ser Asn Gly Ser Thr Asp Leu Val Leu Ile Gly Ala Pro  
450 455 460

His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu  
465 470 475 480

Pro Arg Gly Gln Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Tyr Gly  
485 490 495

Glu Gln Gly Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu  
500 505 510

Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro  
515 520 525

Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser  
530 535 540

Gly Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Lys  
545 550 555 560

Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln  
565 570 575

Asp Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly  
580 585 590

His Val Leu Leu Leu Arg Ser Gln Pro Val Leu Arg Val Lys Ala Ile  
595 600 605

Met Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn  
610 615 620

Asp Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu  
625 630 635 640

His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln  
645 650 655

Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser  
660 665 670

Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln  
675 680 685

Val Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro  
690 695 700

Asn Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe  
705 710 715 720

Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val  
725 730 735

Leu Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu  
740 745 750

Lys Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr  
755 760 765

Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu  
770 775 780

Phe Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg  
785 790 795 800

Thr Gln Val Thr Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val  
805 810 815

Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys  
820 825 830

Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser  
835 840 845

Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe  
850 855 860

Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu  
865 870 875 880

Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn  
885 890 895

Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met  
900 905 910

Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala  
915 920 925

Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn  
930 935 940

Leu Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val  
945 950 955 960

Arg Leu Asn Gln Thr Val Ile Trp Asp Arg Pro Gln Val Thr Phe Ser  
965 970 975

Glu Asn Leu Ser Ser Thr Cys His Thr Lys Glu Arg Leu Pro Ser His  
980 985 990

Ser Asp Phe Leu Ala Glu Leu Arg Lys Ala Pro Val Val Asn Cys Ser  
995 1000 1005

Ile Ala Val Cys Gln Arg Ile Gln Cys Asp Ile Pro Phe Phe Gly  
1010 1015 1020

Ile Gln Glu Glu Phe Asn Ala Thr Leu Lys Gly Asn Leu Ser Phe  
1025 1030 1035

Asp Trp Tyr Ile Lys Thr Ser His Asn His Leu Leu Ile Val Ser  
1040 1045 1050

Thr Ala Glu Ile Leu Phe Asn Asp Ser Val Phe Thr Leu Leu Pro  
1055 1060 1065

Gly Gln Gly Ala Phe Val Arg Ser Gln Thr Glu Thr Lys Val Glu  
1070 1075 1080

Pro Phe Glu Val Pro Asn Pro Leu Pro Leu Ile Val Gly Ser Ser  
1085 1090 1095

Val Gly Gly Leu Leu Leu Leu Ala Leu Ile Thr Ala Ala Leu Tyr  
1100 1105 1110

Lys Leu Gly Phe Phe Lys Arg Gln Tyr Lys Asp Met Met Ser Glu  
1115 1120 1125

Gly Gly Pro Pro Gly Ala Glu Pro Gln  
1130 1135

<210> 2  
<211> 4740  
<212> DNA  
<213> Homo sapiens

<400> 2  
gaattccgtg gttcctcagt ggtgcctgca acccctgggtt cacctccttc caggttctgg 60  
ctccttccag ccatggctct cagagtcctt ctgttaacag ccttgacctt atgtcatggg 120  
ttcaacttgg acactgaaaa cgcaatgacc ttccaagaga acgcaagggg cttcgggcag 180  
agcgtggtcc agcttcaggg atccagggtg gtgggtggag ccccccagga gatagtggct 240  
gccaaccaaa ggggcagcct ctaccagtgc gactacagca caggctcatg cgagccatc 300  
cgccctgcagg tccccgtgga ggccgtgaac atgtccctgg gcctgtccct ggcagccacc 360

accagccccc	ctcagctgct	ggcctgtgg	cccaccgtgc	accagacttg	cagtgagaac	420
acgtatgtga	aagggctctg	cttcctgttt	ggatccaacc	tacggcagca	gccccagaag	480
ttccccagagg	ccctccgagg	gtgtcctcaa	gaggatagtg	acattgcctt	cttgattgat	540
ggctctggta	gcatcatccc	acatgacttt	cggcggatga	aggagtttgt	ctcaactgtg	600
atggagcaat	taaaaaagtc	caaaaccttg	ttctcttga	tgcagtaactc	tgaagaattc	660
cggattcaact	ttaccttcaa	agagttccag	aacaacccta	acccaagatc	actggtgaag	720
ccaataacgc	agctgcttgg	gccccacac	acggccacgg	gcatccgcaa	agtgg tacga	780
gagctgttta	acatcaccaa	cgagccccga	aagaatgcct	ttaagatcct	agttgtcatc	840
acggatggag	aaaagttgg	cgatcccttg	ggatatgagg	atgtcatccc	tgaggcagac	900
agagagggag	tcattcgcta	cgtcattggg	gtggagatg	ccttccgcag	tgagaaatcc	960
cgc当地	ttaataccat	cgc当地	ccgc当地	atcacgttt	ccaggtgaat	1020
aactttgagg	ctctgaagac	cattcagaac	cagttcggg	agaagatctt	tgc当地	1080
ggta	c当地	c当地	gagcatgaga	tgtctcagga	aggctcagc	1140
gctgccatca	cctctaattgg	ccc当地	agcactgtgg	ggagctatga	ctgggctgg	1200
ggagtcttcc	tatatacatc	aaaggagaaa	agcacctca	tcaacatgac	cagagtggat	1260
tcagacatga	atgatgctta	cttgggat	gctgcccca	tcatcttacg	gaaccgggtg	1320
caaagcctgg	ttctggggc	acctcgat	cagcacatcg	gcctggtagc	gatgttcagg	1380
cagaacactg	gcatgtggg	gtccaa	aatgtcaagg	gcacccagat	cggcgcctac	1440
ttc当地	ccctctgctc	cgtggacgtg	gacagcaacg	gcagcaccga	cctggcctc	1500
atc当地	ccc当地	cgagcagacc	cgagggggcc	aggtgtccgt	gtgccccttg	1560
ccc当地	agagggctcg	gtggcagtgt	gatgtgttc	tctacggg	gcagggccaa	1620
ccctggggcc	gcttggggc	agccctaaca	gtgctgggg	acgtaaatgg	ggacaagctg	1680
acggacgtgg	ccattggggc	ccc当地	gaggacaacc	ggggctgtgt	ttacctgttt	1740
cacggAACCT	caggatctgg	catcagccc	tcccatagcc	agcggatagc	aggctccaag	1800
ctctctccca	ggctccagta	tttggtca	tcactgagtg	ggggccagga	cctcacaatg	1860
gatggactgg	tagacctgac	tgttaggagcc	cagggccacg	tgctgctgct	caggtcccag	1920
ccagta	gagtcaaggc	aatcatggag	ttcaatccc	gggaagtggc	aaggaatgta	1980
tttgagtgta	atgatcaggt	ggtgaaaggc	aaggaagccg	gagaggtcag	agtctgcctc	2040

catgtccaga agagcacacg ggatcggtca agagaaggac agatccagag ttttgtact	2100
tatgacctgg ctctggactc cggccgcccc cattcccgcg ccgttcaa tgagacaaag	2160
aacagcacac gcagacagac acaggtcttgg gggctgaccc agacttgtga gaccctgaaa	2220
ctacagttgc cgaattgcat cgaggaccca gtgagcccc ttgtgctgct cctgaacttc	2280
tctctggtgg gaacgccatt gtctgcttgc gggaaacctcc ggccagtgtct ggcggaggat	2340
gctcagagac tcttcacagc cttgtttccc tttgagaaga attgtggcaa tgacaacatc	2400
tgccaggatg acctcagcat caccttcagt ttcatgagcc tggactgcct cgtgggtgg	2460
gggccccggg agttcaacgt gacagtgact gtgagaaatg atggtgagga ctcctacagg	2520
acacaggtca ctttcttctt cccgcttgc ctgtcctacc ggaagggtgtc cacactccag	2580
aaccagcgct cacagcgatc ctggcgccctg gcctgtgagt ctgcctccctc caccgaagt	2640
tctggggcct tgaagagcac cagctgcagc ataaaccacc ccatcttccc ggaaaactca	2700
gaggtcacct ttaatatcac gtttgatgta gactctaagg cttcccttgg aaacaaactg	2760
ctcctcaagg ccaatgtgac cagtgagaac aacatgccc gaaccaacaa aaccgaattc	2820
caactggagc tgccgggtgaa atatgctgtc tacatggtgg tcaccagcca tggggtctcc	2880
actaaatatac tcaacttcac ggcctcagag aataccagtc gggtcatgca gcatcaatata	2940
caggtcagca acctggggca gaggagcctc cccatcagcc tgggtttctt ggtggccgtc	3000
cggctgaacc agactgtcat atgggaccgc ccccaaggta ctttctccga gaacctctcg	3060
agtacgtgcc acaccaagga ggccttgccc tctcaactccg actttctggc tgagttcgg	3120
aaggcccccg tggtaactg ctccatcgct gtctgccaga gaatccagtg tgacatcccg	3180
ttctttggca tccaggaaga attcaatgta accctcaaag gcaacctctc gtttgactgg	3240
tacatcaaga cctcgataa ccacccctg atcgtgagca cagctgagat cttgtttaac	3300
gattccgtgt tcaccctgct gcccggacag gggcggttg tgaggtccca gacggagacc	3360
aaagtggagc cgttcgaggt ccccaacccc ctgcccgtca tcgtggcag ctctgtcggt	3420
ggactgctgc tcctggccct catcaccgccc ggcgtgtaca agctcggtttt cttcaagcg	3480
caatacaagg acatgatgag tgaagggggc cccccggggg ccgaacccca gtagcggctc	3540
cttcccgaca gagctgcctc tcggtgccca gcaggactct gcccagacca cacgtagccc	3600
ccaggctgct ggacacgtcg gacagcgaag tatccccgac aggacgggt tgggcttcca	3660
tttgggtgtg tgcaagtgtg tatgtgcgtg tgtgcgtgt tgcaagtg tctgtgtgca	3720
agtgtgtgca cgtgtgcgtg tgcgtgcgtg tgcactcgca cgcggatgtg tgagtgtgtg	3780

caagtatgtg agtgtgtcca gtgtgtgtgc gtgtgtccat gtgtgtgcag tgtgtgcatg	3840
tgtgcgagtg tgtgcatgtg tgtgctcagg ggctgtggct cacgtgtgtg actcagagtg	3900
tctctggcgt gtgggtaggt gacggcagcg tagcctctcc ggcagaaggg aactgcctgg	3960
gctcccttgc gcgtggtaa gccgctgctg ggtttcctc cgggagaggg gacggtaat	4020
cctgtgggtg aagagagagg gaaacacagc agcatctctc cactgaaaga agtgggactt	4080
cccgtcgcct gcgagcctgc ggcctgctgg agcctgcgca gcttggatgg atactccatg	4140
agaaaaagccg tgggtgaaac caggagcctc ctccacacca gcgctgatgc ccaataaaga	4200
tgcccactga ggaatcatga agtttcctt ctggattcat ttattatttc aatgtgactt	4260
taatttttg gatggataag cctgtctatg gtacaaaaat cacaaggcat tcaagtgtac	4320
agtggaaaat ctcccttcc agatattcaa gtcacccct taaaggttgt caagattgtg	4380
tttgagggt tccttcagac agattccagg cgatgtgcaa gtgtatgcac gtgtgcacac	4440
accacacaca tacacacaca caagctttt tacacaaatg gtagcataact ttatattgg	4500
ctgtatcttgc ttttttca ccaatatttc tcagacatcg gttcatatta agacataaat	4560
tacttttca ttctttata ccgctgcata gtattccatt gtgtgagtgt accataatgt	4620
atttaccag tcttcttttgc atatactatt ttcatctctt gttattgcat ctgctgagtt	4680
aataatcaa atatatgtca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	4740

<210> 3  
 <211> 1137  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> synthetic

<400> 3

Phe	Asn	Leu	Asp	Thr	Glu	Asn	Ala	Met	Thr	Phe	Gln	Glu	Asn	Ala	Arg
1					5				10				15		

Gly	Phe	Gly	Gln	Ser	Val	Val	Gln	Leu	Gln	Gly	Ser	Arg	Val	Val	Val
					20			25				30			

Gly	Ala	Pro	Gln	Glu	Ile	Val	Ala	Ala	Asn	Gln	Arg	Gly	Ser	Leu	Tyr
						35			40			45			

Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val

50

55

60

Pro Val Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Thr  
65 70 75 80

Thr Ser Pro Pro Gln Leu Leu Ala Cys Gly Pro Thr Val His Gln Thr  
85 90 95

Cys Ser Glu Asn Thr Tyr Val Lys Gly Leu Cys Phe Leu Phe Gly Ser  
100 105 110

Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys  
115 120 125

Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser  
130 135 140

Ile Ile Pro His Asp Phe Arg Arg Met Lys Glu Leu Val Ser Thr Ile  
145 150 155 160

Met Glu Gln Leu Lys Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr  
165 170 175

Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn  
180 185 190

Pro Asn Pro Arg Ser Leu Ile Lys Pro Ile Thr Gln Leu Leu Gly Arg  
195 200 205

Thr His Thr Ala Thr Gly Leu Arg Lys Val Val Arg Glu Leu Phe Asn  
210 215 220

Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Phe Leu Leu  
225 230 235 240

Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile  
245 250 255

Pro Glu Leu Asp Arg Glu Gly Val Ile Arg Tyr Val Leu Gly Phe Gly  
260 265 270

Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Val Ala  
275 280 285

Ser Lys Pro Pro Arg Asp His Val Phe Gln Ala Asn Asn Phe Glu Ala  
290 295 300

Leu Lys Thr Val Gln Asn Gln Leu Arg Glu Lys Ile Phe Ala Ile Glu  
305 310 315 320

Gly Thr Gln Thr Gly Ser Ser Ser Phe Glu His Glu Met Ser Gln  
325 330 335

Glu Gly Phe Ser Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr  
340 345 350

Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys  
355 360 365

Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn  
370 375 380

Asp Ala Tyr Leu Gly Tyr Ala Ala Ala Ile Ile Leu Arg Asn Arg Val  
385 390 395 400

Gln Ser Leu Val Leu Gly Ala Pro Arg Tyr Gln His Ile Gly Leu Val  
405 410 415

Ala Met Phe Arg Gln Asn Thr Gly Met Trp Glu Ser Asn Ala Asn Val  
420 425 430

Lys Gly Thr Gln Ile Gly Ala Tyr Phe Gly Ala Ser Leu Cys Ser Val  
435 440 445

Asp Val Asp Ser Asn Gly Ser Thr Asp Leu Val Leu Ile Gly Ala Pro  
450 455 460

His Tyr Tyr Glu Gln Thr Arg Gly Gln Val Ser Val Cys Pro Leu  
465 470 475 480

Pro Arg Gly Gln Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Tyr Gly  
485 490 495

Glu Gln Gly Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu  
500 505 510

Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro  
515 520 525

Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser  
530 535 540

Gly Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Lys  
545 550 555 560

Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln  
565 570 575

Asp Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly  
580 585 590

His Val Leu Leu Leu Arg Ser Gln Pro Val Leu Arg Val Lys Ala Ile  
595 600 605

Met Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn  
610 615 620

Asp Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu  
625 630 635 640

His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln  
645 650 655

Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser  
660 665 670

Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln  
675 680 685

Val Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro  
690 695 700

Asn Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe  
705 710 715 720

Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val  
725 730 735

Leu Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu  
740 745 750

Lys Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr  
755 760 765

Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu  
770 775 780

Phe Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg  
785 790 795 800

Thr Gln Val Thr Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val  
805 810 815

Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys  
820 825 830

Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser  
835 840 845

Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe  
850 855 860

Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu  
865 870 875 880

Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn  
885 890 895

Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met  
900 905 910

Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala  
915 920 925

Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn  
930 935 940

Leu Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val  
945 950 955 960

Arg Leu Asn Gln Thr Val Ile Trp Asp Arg Pro Gln Val Thr Phe Ser

965

970

975

Glu Asn Leu Ser Ser Thr Cys His Thr Lys Glu Arg Leu Pro Ser His  
980 985 990

Ser Asp Phe Leu Ala Glu Leu Arg Lys Ala Pro Val Val Asn Cys Ser  
995 1000 1005

Ile Ala Val Cys Gln Arg Ile Gln Cys Asp Ile Pro Phe Phe Gly  
1010 1015 1020

Ile Gln Glu Glu Phe Asn Ala Thr Leu Lys Gly Asn Leu Ser Phe  
1025 1030 1035

Asp Trp Tyr Ile Lys Thr Ser His Asn His Leu Leu Ile Val Ser  
1040 1045 1050

Thr Ala Glu Ile Leu Phe Asn Asp Ser Val Phe Thr Leu Leu Pro  
1055 1060 1065

Gly Gln Gly Ala Phe Val Arg Ser Gln Thr Glu Thr Lys Val Glu  
1070 1075 1080

Pro Phe Glu Val Pro Asn Pro Leu Pro Leu Ile Val Gly Ser Ser  
1085 1090 1095

Val Gly Gly Leu Leu Leu Ala Leu Ile Thr Ala Ala Leu Tyr  
1100 1105 1110

Lys Leu Gly Phe Phe Lys Arg Gln Tyr Lys Asp Met Met Ser Glu  
1115 1120 1125

Gly Gly Pro Pro Gly Ala Glu Pro Gln  
1130 1135

<210> 4  
<211> 1137  
<212> PRT  
<213> Artificial sequence

<220>  
<223> synthetic

<400> 4

Phe Asn Leu Asp Thr Glu Asn Ala Met Thr Phe Gln Glu Asn Ala Arg  
1 5 10 15

Gly Phe Gly Gln Ser Val Val Gln Leu Gln Gly Ser Arg Val Val Val  
20 25 30

Gly Ala Pro Gln Glu Ile Val Ala Ala Asn Gln Arg Gly Ser Leu Tyr  
35 40 45

Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val  
50 55 60

Pro Val Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Thr  
65 70 75 80

Thr Ser Pro Pro Gln Leu Leu Ala Cys Gly Pro Thr Val His Gln Thr  
85 90 95

Cys Ser Glu Asn Thr Tyr Val Lys Gly Leu Cys Phe Leu Phe Gly Ser  
100 105 110

Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys  
115 120 125

Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser  
130 135 140

Ile Ile Pro His Asp Phe Arg Arg Met Lys Glu Trp Val Ser Thr Val  
145 150 155 160

Met Glu Gln Leu Lys Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr  
165 170 175

Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn  
180 185 190

Pro Asn Pro Arg Ser Leu Ile Lys Pro Ile Thr Gln Leu Leu Gly Arg  
195 200 205

Thr His Thr Ala Thr Gly Leu Arg Lys Val Val Arg Glu Leu Phe Asn  
210 215 220

Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Phe Leu Leu

225

230

235

240

Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile  
245 250 255

Pro Glu Leu Asp Arg Glu Gly Val Ile Arg Tyr Val Ile Gly Val Gly  
260 265 270

Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Val Ala  
275 280 285

Ser Lys Pro Pro Arg Asp His Val Phe Gln Ile Asn Asn Phe Glu Ala  
290 295 300

Leu Lys Thr Ile Gln Asn Gln Leu Arg Glu Lys Ile Phe Ala Ile Glu  
305 310 315 320

Gly Thr Gln Thr Gly Ser Ser Ser Phe Glu His Glu Met Ser Gln  
325 330 335

Glu Gly Phe Ser Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr  
340 345 350

Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys  
355 360 365

Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn  
370 375 380

Asp Ala Tyr Leu Gly Tyr Ala Ala Ala Ile Ile Leu Arg Asn Arg Val  
385 390 395 400

Gln Ser Leu Val Leu Gly Ala Pro Arg Tyr Gln His Ile Gly Leu Val  
405 410 415

Ala Met Phe Arg Gln Asn Thr Gly Met Trp Glu Ser Asn Ala Asn Val  
420 425 430

Lys Gly Thr Gln Ile Gly Ala Tyr Phe Gly Ala Ser Leu Cys Ser Val  
435 440 445

Asp Val Asp Ser Asn Gly Ser Thr Asp Leu Val Leu Ile Gly Ala Pro  
450 455 460

His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu  
465 470 475 480

Pro Arg Gly Gln Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Tyr Gly  
485 490 495

Glu Gln Gly Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu  
500 505 510

Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro  
515 520 525

Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser  
530 535 540

Gly Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Lys  
545 550 555 560

Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln  
565 570 575

Asp Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly  
580 585 590

His Val Leu Leu Leu Arg Ser Gln Pro Val Leu Arg Val Lys Ala Ile  
595 600 605

Met Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn  
610 615 620

Asp Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu  
625 630 635 640

His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln  
645 650 655

Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser  
660 665 670

Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln  
675 680 685

Val Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro  
690 695 700

Asn Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe  
705 710 715 720

Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val  
725 730 735

Leu Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu  
740 745 750

Lys Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr  
755 760 765

Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu  
770 775 780

Phe Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg  
785 790 795 800

Thr Gln Val Thr Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val  
805 810 815

Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys  
820 825 830

Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser  
835 840 845

Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe  
850 855 860

Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu  
865 870 875 880

Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn  
885 890 895

Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met  
900 905 910

Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala  
915 920 925

Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn  
930 935 940

Leu Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val  
945 950 955 960

Arg Leu Asn Gln Thr Val Ile Trp Asp Arg Pro Gln Val Thr Phe Ser  
965 970 975

Glu Asn Leu Ser Ser Thr Cys His Thr Lys Glu Arg Leu Pro Ser His  
980 985 990

Ser Asp Phe Leu Ala Glu Leu Arg Lys Ala Pro Val Val Asn Cys Ser  
995 1000 1005

Ile Ala Val Cys Gln Arg Ile Gln Cys Asp Ile Pro Phe Phe Gly  
1010 1015 1020

Ile Gln Glu Glu Phe Asn Ala Thr Leu Lys Gly Asn Leu Ser Phe  
1025 1030 1035

Asp Trp Tyr Ile Lys Thr Ser His Asn His Leu Leu Ile Val Ser  
1040 1045 1050

Thr Ala Glu Ile Leu Phe Asn Asp Ser Val Phe Thr Leu Leu Pro  
1055 1060 1065

Gly Gln Gly Ala Phe Val Arg Ser Gln Thr Glu Thr Lys Val Glu  
1070 1075 1080

Pro Phe Glu Val Pro Asn Pro Leu Pro Leu Ile Val Gly Ser Ser  
1085 1090 1095

Val Gly Gly Leu Leu Leu Ala Leu Ile Thr Ala Ala Leu Tyr  
1100 1105 1110

Lys Leu Gly Phe Phe Lys Arg Gln Tyr Lys Asp Met Met Ser Glu  
1115 1120 1125

Gly Gly Pro Pro Gly Ala Glu Pro Gln

1130

1135

<210> 5  
<211> 1137  
<212> PRT  
<213> Artificial sequence

<220>  
<223> synthetic

<400> 5

Phe Asn Leu Asp Thr Glu Asn Ala Met Thr Phe Gln Glu Asn Ala Arg  
1 5 10 15

Gly Phe Gly Gln Ser Val Val Gln Leu Gln Gly Ser Arg Val Val Val  
20 25 30

Gly Ala Pro Gln Glu Ile Val Ala Ala Asn Gln Arg Gly Ser Leu Tyr  
35 40 45

Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val  
50 55 60

Pro Val Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Thr  
65 70 75 80

Thr Ser Pro Pro Gln Leu Leu Ala Cys Gly Pro Thr Val His Gln Thr  
85 90 95

Cys Ser Glu Asn Thr Tyr Val Lys Gly Leu Cys Phe Leu Phe Gly Ser  
100 105 110

Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys  
115 120 125

Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Val Asp Gly Ser Gly Ser  
130 135 140

Ile Ile Pro His Asp Phe Arg Arg Ala Lys Glu Phe Ile Ser Thr Val  
145 150 155 160

Met Glu Gln Leu Lys Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr  
165 170 175

Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn  
180 185 190

Pro Asn Pro Arg Ser Leu Ile Lys Pro Ile Thr Gln Leu Leu Gly Arg  
195 200 205

Thr His Thr Ala Thr Gly Ile Arg Lys Val Val Arg Glu Leu Phe Asn  
210 215 220

Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Ile Leu Ile  
225 230 235 240

Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile  
245 250 255

Pro Glu Ala Asp Arg Glu Gly Val Ile Arg Tyr Val Ile Gly Val Gly  
260 265 270

Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Val Ala  
275 280 285

Ser Lys Pro Pro Arg Asp His Val Phe Gln Ile Asn Asn Phe Glu Ala  
290 295 300

Leu Lys Thr Ile Gln Asn Gln Leu Arg Glu Lys Ile Phe Ala Ile Glu  
305 310 315 320

Gly Thr Gln Thr Gly Ser Ser Ser Phe Glu His Glu Met Ser Gln  
325 330 335

Glu Gly Phe Ser Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr  
340 345 350

Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys  
355 360 365

Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn  
370 375 380

Asp Ala Tyr Leu Gly Tyr Ala Ala Ala Ile Ile Leu Arg Asn Arg Val  
385 390 395 400

Gln Ser Leu Val Leu Gly Ala Pro Arg Tyr Gln His Ile Gly Leu Val

405

410

415

Ala Met Phe Arg Gln Asn Thr Gly Met Trp Glu Ser Asn Ala Asn Val  
420 425 430

Lys Gly Thr Gln Ile Gly Ala Tyr Phe Gly Ala Ser Leu Cys Ser Val  
435 440 445

Asp Val Asp Ser Asn Gly Ser Thr Asp Leu Val Leu Ile Gly Ala Pro  
450 455 460

His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu  
465 470 475 480

Pro Arg Gly Gln Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Tyr Gly  
485 490 495

Glu Gln Gly Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu  
500 505 510

Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro  
515 520 525

Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser  
530 535 540

Gly Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Lys  
545 550 555 560

Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln  
565 570 575

Asp Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly  
580 585 590

His Val Leu Leu Leu Arg Ser Gln Pro Val Leu Arg Val Lys Ala Ile  
595 600 605

Met Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn  
610 615 620

Asp Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu  
625 630 635 640

His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln  
645 650 655

Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser  
660 665 670

Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln  
675 680 685

Val Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro  
690 695 700

Asn Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe  
705 710 715 720

Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val  
725 730 735

Leu Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu  
740 745 750

Lys Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr  
755 760 765

Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu  
770 775 780

Phe Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg  
785 790 795 800

Thr Gln Val Thr Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val  
805 810 815

Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys  
820 825 830

Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser  
835 840 845

Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe  
850 855 860

Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu  
865 870 875 880

Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn  
885 890 895

Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met  
900 905 910

Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala  
915 920 925

Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn  
930 935 940

Leu Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val  
945 950 955 960

Arg Leu Asn Gln Thr Val Ile Trp Asp Arg Pro Gln Val Thr Phe Ser  
965 970 975

Glu Asn Leu Ser Ser Thr Cys His Thr Lys Glu Arg Leu Pro Ser His  
980 985 990

Ser Asp Phe Leu Ala Glu Leu Arg Lys Ala Pro Val Val Asn Cys Ser  
995 1000 1005

Ile Ala Val Cys Gln Arg Ile Gln Cys Asp Ile Pro Phe Phe Gly  
1010 1015 1020

Ile Gln Glu Glu Phe Asn Ala Thr Leu Lys Gly Asn Leu Ser Phe  
1025 1030 1035

Asp Trp Tyr Ile Lys Thr Ser His Asn His Leu Leu Ile Val Ser  
1040 1045 1050

Thr Ala Glu Ile Leu Phe Asn Asp Ser Val Phe Thr Leu Leu Pro  
1055 1060 1065

Gly Gln Gly Ala Phe Val Arg Ser Gln Thr Glu Thr Lys Val Glu  
1070 1075 1080

Pro Phe Glu Val Pro Asn Pro Leu Pro Leu Ile Val Gly Ser Ser  
1085 1090 1095

Val Gly Gly Leu Leu Leu Leu Ala Leu Ile Thr Ala Ala Leu Tyr  
1100 1105 1110

Lys Leu Gly Phe Phe Lys Arg Gln Tyr Lys Asp Met Met Ser Glu  
1115 1120 1125

Gly Gly Pro Pro Gly Ala Glu Pro Gln  
1130 1135

<210> 6  
<211> 1137  
<212> PRT  
<213> Artificial sequence

<220>  
<223> synthetic

<400> 6

Phe Asn Leu Asp Thr Glu Asn Ala Met Thr Phe Gln Glu Asn Ala Arg  
1 5 10 15

Gly Phe Gly Gln Ser Val Val Gln Leu Gln Gly Ser Arg Val Val Val  
20 25 30

Gly Ala Pro Gln Glu Ile Val Ala Ala Asn Gln Arg Gly Ser Leu Tyr  
35 40 45

Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val  
50 55 60

Pro Val Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Thr  
65 70 75 80

Thr Ser Pro Pro Gln Leu Leu Ala Cys Gly Pro Thr Val His Gln Thr  
85 90 95

Cys Ser Glu Asn Thr Tyr Val Lys Gly Leu Cys Phe Leu Phe Gly Ser  
100 105 110

Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys  
115 120 125

Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser  
130 135 140

Ile Ile Pro His Asp Phe Arg Arg Met Lys Glu Phe Val Ser Thr Val  
145 150 155 160

Met Glu Gln Leu Lys Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr  
165 170 175

Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn  
180 185 190

Pro Asn Pro Arg Ser Leu Val Lys Pro Ile Thr Gln Leu Leu Gly Arg  
195 200 205

Thr His Thr Ala Thr Gly Val Arg Lys Val Ile Arg Glu Leu Leu Asn  
210 215 220

Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Ile Val Ile  
225 230 235 240

Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile  
245 250 255

Pro Glu Ala Asp Arg Glu Gly Val Ile Arg Tyr Val Ile Gly Val Gly  
260 265 270

Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Ile Ala  
275 280 285

Ser Lys Pro Pro Arg Asp His Val Phe Gln Val Asn Asn Phe Glu Ala  
290 295 300

Leu Lys Thr Ile Gln Asn Gln Leu Arg Glu Lys Ile Phe Ala Ile Glu  
305 310 315 320

Gly Thr Gln Thr Gly Ser Ser Ser Phe Glu His Glu Met Ser Gln  
325 330 335

Glu Gly Phe Ser Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr  
340 345 350

Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys  
355 360 365

Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn  
370 375 380

Asp Ala Tyr Leu Gly Tyr Ala Ala Ala Ile Ile Leu Arg Asn Arg Val  
385 390 395 400

Gln Ser Leu Val Leu Gly Ala Pro Arg Tyr Gln His Ile Gly Leu Val  
405 410 415

Ala Met Phe Arg Gln Asn Thr Gly Met Trp Glu Ser Asn Ala Asn Val  
420 425 430

Lys Gly Thr Gln Ile Gly Ala Tyr Phe Gly Ala Ser Leu Cys Ser Val  
435 440 445

Asp Val Asp Ser Asn Gly Ser Thr Asp Leu Val Leu Ile Gly Ala Pro  
450 455 460

His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu  
465 470 475 480

Pro Arg Gly Gln Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Tyr Gly  
485 490 495

Glu Gln Gly Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu  
500 505 510

Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro  
515 520 525

Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser  
530 535 540

Gly Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Lys  
545 550 555 560

Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln  
565 570 575

Asp Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly

580

585

590

His Val Leu Leu Leu Arg Ser Gln Pro Val Leu Arg Val Lys Ala Ile  
595 600 605

Met Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn  
610 615 620

Asp Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu  
625 630 635 640

His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln  
645 650 655

Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser  
660 665 670

Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln  
675 680 685

Val Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro  
690 695 700

Asn Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe  
705 710 715 720

Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val  
725 730 735

Leu Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu  
740 745 750

Lys Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr  
755 760 765

Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu  
770 775 780

Phe Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg  
785 790 795 800

Thr Gln Val Thr Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val  
805 810 815

Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys  
820 825 830

Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser  
835 840 845

Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe  
850 855 860

Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu  
865 870 875 880

Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn  
885 890 895

Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met  
900 905 910

Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala  
915 920 925

Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn  
930 935 940

Leu Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val  
945 950 955 960

Arg Leu Asn Gln Thr Val Ile Trp Asp Arg Pro Gln Val Thr Phe Ser  
965 970 975

Glu Asn Leu Ser Ser Thr Cys His Thr Lys Glu Arg Leu Pro Ser His  
980 985 990

Ser Asp Phe Leu Ala Glu Leu Arg Lys Ala Pro Val Val Asn Cys Ser  
995 1000 1005

Ile Ala Val Cys Gln Arg Ile Gln Cys Asp Ile Pro Phe Phe Gly  
1010 1015 1020

Ile Gln Glu Glu Phe Asn Ala Thr Leu Lys Gly Asn Leu Ser Phe  
1025 1030 1035

Asp Trp Tyr Ile Lys Thr Ser His Asn His Leu Leu Ile Val Ser  
1040 1045 1050

Thr Ala Glu Ile Leu Phe Asn Asp Ser Val Phe Thr Leu Leu Pro  
1055 1060 1065

Gly Gln Gly Ala Phe Val Arg Ser Gln Thr Glu Thr Lys Val Glu  
1070 1075 1080

Pro Phe Glu Val Pro Asn Pro Leu Pro Leu Ile Val Gly Ser Ser  
1085 1090 1095

Val Gly Gly Leu Leu Leu Leu Ala Leu Ile Thr Ala Ala Leu Tyr  
1100 1105 1110

Lys Leu Gly Phe Phe Lys Arg Gln Tyr Lys Asp Met Met Ser Glu  
1115 1120 1125

Gly Gly Pro Pro Gly Ala Glu Pro Gln  
1130 1135

<210> 7  
<211> 10  
<212> PRT  
<213> Artificial sequence

<220>  
<223> stability sequence

<220>  
<221> MISC\_FEATURE  
<222> (3)..(6)  
<223> "Xaa" at positions 3 through 6 can be any amino acid.

<400> 7

Met Gly Xaa Xaa Xaa Xaa Gly Gly Pro Pro  
1 5 10

<210> 8  
<211> 7  
<212> PRT  
<213> Artificial sequence

<220>  
<223> example

<400> 8

Leu Val Leu Val Leu Val Leu  
1 5

<210> 9

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> example

<400> 9

Leu Pro Leu Pro Leu Val Leu  
1 5

<210> 10

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> example

<400> 10

Leu Pro Leu Pro Leu Pro Leu  
1 5

<210> 11

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> example

<400> 11

Leu Pro Pro Pro Leu Val Leu  
1 5

<210> 12

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> example

<400> 12

Leu Pro Pro Val Leu Pro Pro  
1 5

<210> 13  
<211> 7  
<212> PRT  
<213> Artificial sequence

<220>  
<223> example

<400> 13

Pro Pro Leu Pro Pro Val Pro  
1 5